Atty. Dkt. No. 039386-0307
(PF-0544USN)

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

21. (Cancelled)

22. (Cancelled)

23. (Cancelled)

24. (Cancelled)

25. (Currently Amended) An isolated polynucleotide of claim ~~24~~ 31 comprising a polynucleotide sequence ~~selected from the group consisting~~ of SEQ ID NO: ~~7-12~~ 11.

26. (Currently Amended) A ~~recombinant~~ polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim ~~23~~ 31.

27. (Currently Amended) A cell transformed with a ~~recombinant~~ polynucleotide of claim 26.

28. (Currently Amended) A method of producing a polypeptide ~~of claim 21~~, the method comprising:

a) culturing a cell of claim 26 under conditions suitable for expression of the polypeptide, ~~wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 21,~~ and

b) recovering the polypeptide so expressed.

29. (Currently Amended) A method of claim 28, wherein the polypeptide comprises an amino acid sequence ~~selected from the group consisting~~ of SEQ ID NO: ~~1-6~~ 5.

30. (Cancelled)

31. (Currently Amended) An isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising a polynucleotide sequence ~~selected from the group consisting~~ of SEQ ID NO: ~~7-12~~ 11,

(b) a polynucleotide comprising a ~~naturally occurring~~ polynucleotide sequence having at least 90% ~~identical~~ sequence identity to ~~a polynucleotide sequence selected from the group consisting of~~ SEQ ID NO: ~~7-12~~ 11,

(c) a polynucleotide complementary to a polynucleotide of (a) or (b), and

(d) ~~a polynucleotide complementary to a polynucleotide of b), and c)~~ an RNA equivalent of (a) ~~d)~~ (c).

32. (Currently Amended) A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 31, the method comprising:

(a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides ~~comprising a sequence~~ complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

(b) detecting the presence or absence of said hybridization complex, and,

optionally, if present, the amount thereof.

33. A method of claim 32, wherein the probe comprises at least 60 contiguous nucleotides.

34. (Currently Amended) A method of detecting a target polynucleotide in a sample comprising nucleic acid, said target polynucleotide having a sequence of a polynucleotide of claim 31, the method comprising:

(a) amplifying said target polynucleotide or fragment thereof if present in the sample nucleic acid using polymerase chain reaction amplification, and

(b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

35. (Currently Amended) A composition comprising a ~~polypeptide~~ polynucleotide of claim ~~21~~ 31 and a pharmaceutically acceptable excipient.

36. (Cancelled)

37. (Cancelled)

38. (Cancelled)

39. (Currently Amended) A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim ~~25~~ 31, the method comprising:

(a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

(b) detecting altered expression of the target polynucleotide, and

(c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound ~~and~~ with the expression of the target polynucleotide in the absence of the compound.

40. (Currently Amended) A method of assessing toxicity of a test compound, the method comprising:

(a) treating a biological sample containing nucleic acids with the test compound,

(b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 31 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 31 ~~or fragment thereof~~,

(c) quantifying the amount of hybridization complex, and

(d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.